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			959	5	55.6	976	2	Q73SX6_MYCPA	Q73sx6 m
960	5	55.6	979	2	Q4DKR7_TRYCR	Q4dkr7		trypanosoma	
961	5	55.6	981	2	Q5AQL1_EMENI	Q5aql1		aspergillus	
962	5	55.6	982	2	Q54ZK5_DICDI	Q54zk5		dictyosteli	
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964	5	55.6	982	2	Q6UGD2_BPSP6	Q6ugd2		enterobacte	
965	5	55.6	989	2	Q4UGW0_THEAN	Q4ugw0		theileria a	
966	5	55.6	991	2	Q72SC6_LEPIC	Q72sc6		leptospira	
967	5	55.6	991	2	Q8F398_LEPIN	Q8f398		leptospira	
968	5	55.6	994	2	Q6CHE0_YARLI	Q6che0		yarrowia li	
969	5	55.6	1002	2	Q8EFG0_SHEON	Q8efg0		shewanella	
970	5	55.6	1003	2	Q9AHP2_9ACTO	Q9ahp2		arcanobacte	
971	5	55.6	1014	2	Q4Q946_LEIMA	Q4q946		leishmania	
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974	5	55.6	1019	2	Q2PJW0_ENTFC	Q2pjw0		enterococcu	
975	5	55.6	1022	2	O61907_CAEEL	O61907		caenorhabdi	
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990	5	55.6	1088	2	Q6ZUM6_HUMAN	Q6zum6		homo sapien	
991	5	55.6	1104	2	Q7MZ50_PHOLL	Q7mz50		photorhabdu	
992	5	55.6	1108	2	Q4ESI0_LISMO	Q4esi0		listeria mo	
993	5	55.6	1113	2	Q511P5_ENTHI	Q511p5		entamoeba h	
994	5	55.6	1117	2	Q388R2_9TRYP	Q388r2		trypanosoma	
995	5	55.6	1138	2	Q4H7T0_9DEIO	Q4h7t0		deinococcus	
996	5	55.6	1144	2	Q54BG8_DICDI	Q54bg8		dictyosteli	
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999	5	55.6	1144	2	Q55D49_DICDI	Q55d49		dictyosteli	
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## ALIGNMENTS

### RESULT 1

VHR2\_CAMPM

ID VHR2\_CAMPM STANDARD; PRT; 150 AA.

AC P68643; Q8V2Z8;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.

DT 07-DEC-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Probable host range protein 2.  
 GN OrderedLocusNames=CMLV019;  
 OS Camelpox virus (strain M-96).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=203173;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=22031204; PubMed=12033760; DOI=10.1006/viro.2001.1343;  
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Sandybaev N.T.,  
 RA Kerembekova U.Z., Zaitsev V.L., Kutish G.F., Rock D.L.;  
 RT "The genome of camelpox virus."  
 RL Virology 295:1-9(2002).  
 CC -!- FUNCTION: Plays a role for multiplication of the virus in  
 CC different cell types (By similarity).  
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
 CC -----  
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 CC -----  
 DR EMBL; AF438165; AAL73726.1; -; Genomic\_DNA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 FT CHAIN 1 150 Probable host range protein 2.  
 FT /FTId=PRO\_0000099390.  
 SQ SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;  
  
 Query Match 100.0%; Score 9; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 KVDDTFYYV 9  
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 Db 74 KVDDTFYYV 82

## RESULT 2

## VHR2\_CAMPS

ID VHR2\_CAMPS STANDARD; PRT; 150 AA.  
 AC P68642; Q8V2Z8;  
 DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 07-DEC-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Probable host range protein 2.  
 GN OrderedLocusNames=CMPI9L;  
 OS Camelpox virus (strain CMS).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=203172;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX PubMed=11907336;  
 RA Gubser C., Smith G.L.;  
 RT "The sequence of camelpox virus shows it is most closely related to  
 RT variola virus, the cause of smallpox."  
 RL J. Gen. Virol. 83:855-872(2002).  
 CC -!- FUNCTION: Plays a role for multiplication of the virus in  
 CC different cell types (By similarity).  
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
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CC -----

DR EMBL; AY009089; AAG37475.1; -; Genomic\_DNA.

DR InterPro; IPR004967; Pox\_C7\_F8A.

DR Pfam; PF03287; Pox\_C7\_F8A; 1.

DR PIRSF; PIRSF003779; VAC\_C7L; 1.

FT CHAIN 1 150 Probable host range protein 2.

FT /FTId=PRO\_0000099391.

SQ SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9

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Db 74 KVDDTFYYV 82

### RESULT 3

#### VHR2\_VACCA

ID VHR2\_VACCA STANDARD; PRT; 150 AA.

AC P68598; P17363; Q76ZY7;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.

DT 07-DEC-2004, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Host range protein 2.

GN OrderedLocusNames=MVA018L, ACAM3000\_MVA\_018;

OS Vaccinia virus (strain Ankara) (VACV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI\_TaxID=126794;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=98263813; PubMed=9601507; DOI=10.1006/viro.1998.9123;

RA Antoine G., Scheiflinger F., Dorner F., Falkner F.G.;

RT "The complete genomic sequence of the modified vaccinia Ankara strain:

RT comparison with other orthopoxviruses.";

RL Virology 244:365-396(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Isolate Acambis 3000;

RA Esposito J.J., Frace M., Sammons S.A., Olsen-Rasmussen M.S.,

RA Osborne J., Khristova M., Wohlhueter R.M.;

RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Plays a role for multiplication of the virus in

CC different cell types (By similarity).

CC -!- SIMILARITY: Belongs to the poxviruses C7 family.

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CC -----

DR EMBL; U94848; AAB96405.1; -; Genomic\_DNA.

DR EMBL; AY603355; AAT10416.1; -; Genomic\_DNA.

DR PIR; A33348; WZVZB1.

DR InterPro; IPR004967; Pox\_C7\_F8A.

DR Pfam; PF03287; Pox\_C7\_F8A; 1.

DR PIRSF; PIRSF003779; VAC\_C7L; 1.

KW Early protein.

FT CHAIN 1 150 Host range protein 2.

FT /FTId=PRO\_0000099386.

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Query Match 100.0%; Score 9; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
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Db 74 KVDDTFYYV 82

## RESULT 4

## VHR2\_VACCC

ID VHR2\_VACCC STANDARD; PRT; 150 AA.  
AC P68599; P17363;  
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.  
DT 07-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE Host range protein 2.  
GN ORFNames=C7L;  
OS Vaccinia virus (strain Copenhagen) (VACV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10249;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=91021027; PubMed=2219722;  
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
RA Paoletti E.;  
RT "The complete DNA sequence of vaccinia virus.";  
RL Virology 179:247-266(1990).  
RN [2]  
RP COMPLETE GENOME.  
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
RA Paoletti E.;  
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";  
RL Virology 179:517-563(1990).  
CC -!- FUNCTION: Plays a role for multiplication of the virus in  
CC different cell types (By similarity).  
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
CC -----  
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CC -----  
DR EMBL; M35027; AAA47993.1; -; Genomic\_DNA.  
DR PIR; A33348; WZVZB1.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
KW Early protein.  
FT CHAIN 1 150 Host range protein 2.  
FT /FTid=PRO\_0000099387.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
|||||||  
Db 74 KVDDTFYYV 82

## RESULT 5

## VHR2\_VACCV

ID VHR2\_VACCV STANDARD; PRT; 150 AA.  
AC P68600; P17363; Q76ZY7;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.  
DT 07-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Host range protein 2.  
GN OrderedLocusNames=VACWR021; ORFNames=C7L;  
OS Vaccinia virus (strain Western Reserve / WR) (VACV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10254;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=89073756; PubMed=2849238;  
RA Kotwal G.J., Moss B.;  
RT "Analysis of a large cluster of nonessential genes deleted from a  
RT vaccinia virus terminal transposition mutant.";  
RL Virology 167:524-537(1988).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RA Esposito J.J., Frace A.M., Sammons S.A., Olsen-Rasmussen M.,  
RA Osborne J., Wohlhueter R.;  
RT "Sequencing of the coding region of Vaccinia-WR to an average 9-fold  
RT redundancy and an error rate of 0.16/10kb.";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP FUNCTION.  
RX MEDLINE=91021030; PubMed=2171207;  
RA Perkus M.E., Goebel S.J., Davis S.W., Johnson G.P., Limbach K.,  
RA Norton E.K., Paoletti E.;  
RT "Vaccinia virus host range genes.";  
RL Virology 179:276-286(1990).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=93329391; PubMed=8336123;  
RA Oguiura N., Spehner D., Drillien R.;  
RT "Detection of a protein encoded by the vaccinia virus C7L open reading  
RT frame and study of its effect on virus multiplication in different  
RT cell lines.";  
RL J. Gen. Virol. 74:1409-1413(1993).  
CC -!- FUNCTION: Plays a role for multiplication of the virus in  
CC different cell types.  
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
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CC -----  
DR EMBL; M22812; AAA69601.1; -; Genomic\_DNA.  
DR EMBL; AY243312; AAO89300.1; -; Genomic\_DNA.  
DR PIR; A33348; WZVZB1.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
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DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
KW Early protein.  
FT CHAIN 1 150 Host range protein 2.  
FT /FTId=PRO\_0000099388.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
| | | | | | | |  
Db 74 KVDDTFYYV 82

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960	5	55.6	979	2	Q4DKR7_TRYCR			Q4dkr7 trypanosoma	
961	5	55.6	981	2	Q5AQL1_EMENI			Q5aql1 aspergillus	
962	5	55.6	982	2	Q54ZK5_DICDI			Q54zk5 dictyosteli	
963	5	55.6	982	2	Q2WC39_9VIRU			Q2wc39 enterobacte	
964	5	55.6	982	2	Q6UGD2_BPSP6			Q6ugd2 enterobacte	
965	5	55.6	989	2	Q4UGW0_THEAN			Q4ugw0 theileria a	
966	5	55.6	991	2	Q72SC6_LEPIC			Q72sc6 leptospira	
967	5	55.6	991	2	Q8F398_LEPIN			Q8f398 leptospira	
968	5	55.6	994	2	Q6CHE0_YARLI			Q6che0 yarrowia li	
969	5	55.6	1002	2	Q8EFG0_SHEON			Q8efg0 shewanella	
970	5	55.6	1003	2	Q9AHP2_9ACTO			Q9ahp2 arcanobacte	
971	5	55.6	1014	2	Q4Q946_LEIMA			Q4q946 leishmania	
972	5	55.6	1019	2	Q4Z9Z8_9CAUD			Q4z9z8 bacterioph	
973	5	55.6	1019	2	Q6Y7Q4_9CAUD			Q6y7q4 staphylococ	
974	5	55.6	1019	2	Q2PJW0_ENTFC			Q2pjw0 enterococcu	
975	5	55.6	1022	2	O61907_CAEEL			O61907 caenorhabdi	
976	5	55.6	1023	2	Q2T7E3_BURTH			Q2t7e3 burkholderi	
977	5	55.6	1028	2	Q5TML1_ANOGA			Q5tml1 anopheles g	
978	5	55.6	1034	2	Q6CX56_KLULA			Q6cx56 kluyveromyc	
979	5	55.6	1042	2	Q6D806_ERWCT			Q6d806 erwinia car	
980	5	55.6	1044	2	Q9ZH24_PSEAE			Q9zh24 pseudomonas	
981	5	55.6	1045	2	Q9RG59_PSEAE			Q9rg59 pseudomonas	
982	5	55.6	1046	2	Q5A115_CANAL			Q5a115 candida alb	
983	5	55.6	1046	2	Q9ZNG8_PSEAE			Q9zng8 pseudomonas	
984	5	55.6	1053	2	Q6FQA8_CANGA			Q6fqa8 candida gla	
985	5	55.6	1070	2	Q7R2W4_GIALA			Q7r2w4 giardia lam	
986	5	55.6	1071	2	Q2Z867_9GAMM			Q2z867 shewanella	
987	5	55.6	1080	2	Q69PR5_ORYSA			Q69pr5 oryza sativ	
988	5	55.6	1083	2	Q43ZL3_SOLUS			Q43zl3 solibacter	
989	5	55.6	1084	2	Q2KEZ1_MAGGR			Q2kez1 magnaporthe	
990	5	55.6	1088	2	Q6ZUM6_HUMAN			Q6zum6 homo sapien	
991	5	55.6	1104	2	Q7MZ50_PHOLL			Q7mz50 photorhabdu	
992	5	55.6	1108	2	Q4ESI0_LISMO			Q4esi0 listeria mo	
993	5	55.6	1113	2	Q511P5_ENTHI			Q511p5 entamoeba h	
994	5	55.6	1117	2	Q388R2_9TRYP			Q388r2 trypanosoma	
995	5	55.6	1138	2	Q4H7T0_9DEIO			Q4h7t0 deinococcus	
996	5	55.6	1144	2	Q54BG8_DICDI			Q54bg8 dictyosteli	
997	5	55.6	1144	2	Q54ZA1_DICDI			Q54za1 dictyosteli	
998	5	55.6	1144	2	Q552I5_DICDI			Q552i5 dictyosteli	
999	5	55.6	1144	2	Q55D49_DICDI			Q55d49 dictyosteli	
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## ALIGNMENTS

### RESULT 1

VHR2\_CAMPM

ID VHR2\_CAMPM STANDARD; PRT; 150 AA.

AC P68643; Q8V2Z8;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.

DT 07-DEC-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Probable host range protein 2.  
 GN OrderedLocusNames=CMLV019;  
 OS Camelpox virus (strain M-96).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=203173;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=22031204; PubMed=12033760; DOI=10.1006/viro.2001.1343;  
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Sandybaev N.T.,  
 RA Kerembekova U.Z., Zaitsev V.L., Kutish G.F., Rock D.L.;  
 RT "The genome of camelpox virus."  
 RL Virology 295:1-9(2002).  
 CC -!- FUNCTION: Plays a role for multiplication of the virus in  
 CC different cell types (By similarity).  
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 CC -----  
 DR EMBL; AF438165; AAL73726.1; -; Genomic\_DNA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 FT CHAIN 1 150 Probable host range protein 2.  
 FT /FTId=PRO\_0000099390.  
 SQ SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;  
  
 Query Match 100.0%; Score 9; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 KVDDTFYYV 9  
 |||||  
 Db 74 KVDDTFYYV 82

## RESULT 2

## VHR2\_CAMPS

ID VHR2\_CAMPS STANDARD; PRT; 150 AA.  
 AC P68642; Q8V2Z8;  
 DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 07-DEC-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Probable host range protein 2.  
 GN OrderedLocusNames=CMF19L;  
 OS Camelpox virus (strain CMS).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=203172;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX PubMed=11907336;  
 RA Gubser C., Smith G.L.;  
 RT "The sequence of camelpox virus shows it is most closely related to  
 RT variola virus, the cause of smallpox."  
 RL J. Gen. Virol. 83:855-872(2002).  
 CC -!- FUNCTION: Plays a role for multiplication of the virus in  
 CC different cell types (By similarity).  
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
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CC -----

DR EMBL; AY009089; AAG37475.1; -; Genomic\_DNA.

DR InterPro; IPR004967; Pox\_C7\_F8A.

DR Pfam; PF03287; Pox\_C7\_F8A; 1.

DR PIRSF; PIRSF003779; VAC\_C7L; 1.

FT CHAIN 1 150 Probable host range protein 2..

FT /FTId=PRO\_0000099391.

SQ SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9

|||||||

Db 74 KVDDTFYYV 82

### RESULT 3

#### VHR2\_VACCA

ID VHR2\_VACCA STANDARD; PRT; 150 AA.

AC P68598; P17363; Q76ZY7;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.

DT 07-DEC-2004, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Host range protein 2.

GN OrderedLocusNames=MVA018L, ACAM3000\_MVA\_018;

OS Vaccinia virus (strain Ankara) (VACV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI\_TaxID=126794;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=98263813; PubMed=9601507; DOI=10.1006/viro.1998.9123;

RA Antoine G., Scheiflinger F., Dorner F., Falkner F.G.;

RT "The complete genomic sequence of the modified vaccinia Ankara strain:

RT comparison with other orthopoxviruses.";

RL Virology 244:365-396(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Isolate Acambis 3000;

RA Esposito J.J., Frace M., Sammons S.A., Olsen-Rasmussen M.S.,

RA Osborne J., Khristova M., Wohlhueter R.M.;

RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Plays a role for multiplication of the virus in

CC different cell types (By similarity).

CC -!- SIMILARITY: Belongs to the poxviruses C7 family.

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CC -----

DR EMBL; U94848; AAB96405.1; -; Genomic\_DNA.

DR EMBL; AY603355; AAT10416.1; -; Genomic\_DNA.

DR PIR; A33348; WZVZB1.

DR InterPro; IPR004967; Pox\_C7\_F8A.

DR Pfam; PF03287; Pox\_C7\_F8A; 1.

DR PIRSF; PIRSF003779; VAC\_C7L; 1.

KW Early protein.

FT CHAIN 1 150 Host range protein 2.

FT /FTId=PRO\_0000099386.

SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;



Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
|||||  
Db 74 KVDDTFYYV 82

## RESULT 4

## VHR2\_VACCC

ID VHR2\_VACCC STANDARD; PRT; 150 AA.  
AC P68599; P17363;  
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.  
DT 07-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE Host range protein 2.  
GN ORFNames=C7L;  
OS Vaccinia virus (strain Copenhagen) (VACV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10249;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=91021027; PubMed=2219722;  
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
RA Paoletti E.;  
RT "The complete DNA sequence of vaccinia virus.";  
RL Virology 179:247-266(1990).  
RN [2]  
RP COMPLETE GENOME.  
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
RA Paoletti E.;  
RT "Appendix to 'The complete DNA sequence of vaccinia virus'. ";  
RL Virology 179:517-563(1990).  
CC -!- FUNCTION: Plays a role for multiplication of the virus in  
CC different cell types (By similarity).  
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
CC -----  
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CC -----  
DR EMBL; M35027; AAA47993.1; -; Genomic\_DNA.  
DR PIR; A33348; WZVZB1.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
KW Early protein.  
FT CHAIN 1 150 Host range protein 2.  
FT /FTId=PRO\_0000099387.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
|||||  
Db 74 KVDDTFYYV 82

## RESULT 5

## VHR2\_VACCV

ID VHR2\_VACCV STANDARD; PRT; 150 AA.  
AC P68600; P17363; Q76ZY7;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.  
DT 07-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Host range protein 2.  
GN OrderedLocusNames=VACWR021; ORFNames=C7L;  
OS Vaccinia virus (strain Western Reserve / WR) (VACV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10254;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=89073756; PubMed=2849238;  
RA Kotwal G.J., Moss B.;  
RT "Analysis of a large cluster of nonessential genes deleted from a  
RT vaccinia virus terminal transposition mutant.";  
RL Virology 167:524-537(1988).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RA Esposito J.J., Frace A.M., Sammons S.A., Olsen-Rasmussen M.,  
RA Osborne J., Wohlhueter R.;  
RT "Sequencing of the coding region of Vaccinia-WR to an average 9-fold  
RT redundancy and an error rate of 0.16/10kb.";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP FUNCTION.  
RX MEDLINE=91021030; PubMed=2171207;  
RA Perkus M.E., Goebel S.J., Davis S.W., Johnson G.P., Limbach K.,  
RA Norton E.K., Paoletti E.;  
RT "Vaccinia virus host range genes.";  
RL Virology 179:276-286(1990).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=93329391; PubMed=8336123;  
RA Oguiura N., Spehner D., Drillien R.;  
RT "Detection of a protein encoded by the vaccinia virus C7L open reading  
RT frame and study of its effect on virus multiplication in different  
RT cell lines.";  
RL J. Gen. Virol. 74:1409-1413(1993).  
CC -!- FUNCTION: Plays a role for multiplication of the virus in  
CC different cell types.  
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
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CC -----  
DR EMBL; M22812; AAA69601.1; -; Genomic\_DNA.  
DR EMBL; AY243312; AAO89300.1; -; Genomic\_DNA.  
DR PIR; A33348; WZVZB1.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
KW Early protein.  
FT CHAIN 1 150 Host range protein 2.  
FT /FTid=PRO\_0000099388.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
|||  
Db 74 KVDDTFYYV 82

## RESULT 6

## VHR2\_VARV

ID VHR2\_VARV STANDARD; PRT; 150 AA.  
AC P33860;  
DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.  
DT 01-FEB-1994, sequence version 1.  
DT 07-FEB-2006, entry version 30.  
DE Host range protein 2.  
GN ORFNames=C7L, B15L, D8L;  
OS Variola virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10255;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=India-1967 / Isolate Ind3;  
RX MEDLINE=93202281; PubMed=8384129; DOI=10.1016/0014-5793(93)80041-R;  
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;  
RT "Genes of variola and vaccinia viruses necessary to overcome the host  
RT protective mechanisms.";  
RL FEBS Lett. 319:80-83(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=Bangladesh-1975;  
RX MEDLINE=94088747; PubMed=8264798; DOI=10.1038/366748a0;  
RA Massung R.F., Esposito J.J., Liu L.I., Qi J., Utterback T.R.,  
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,  
RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,  
RA Venter C.J.;  
RT "Potential virulence determinants in terminal regions of variola  
RT smallpox virus genome.";  
RL Nature 366:748-751(1993).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=Congo-1965, Garcia-1966, and Somalia-1977;  
RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,  
RA Totmenin A.V., Shchelkunov S.N., Esposito J.J.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Plays a role for multiplication of the virus in  
CC different cell types (By similarity).  
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
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CC -----  
DR EMBL; X69198; CAA48949.1; -; Genomic\_DNA.  
DR EMBL; L22579; AAA60756.1; -; Genomic\_DNA.  
DR EMBL; U18340; AAA69419.1; -; Genomic\_DNA.  
DR EMBL; U18337; AAA69313.1; -; Genomic\_DNA.  
DR EMBL; U18338; AAA69354.1; -; Genomic\_DNA.  
DR PIR; F72151; F72151.  
DR PIR; H36837; H36837.  
DR PIR; T28446; T28446.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
FT CHAIN 1 150 Host range protein 2.  
FT /FTId=PRO\_0000099389.  
SQ SEQUENCE 150 AA; 18027 MW; 50FDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
|||||  
Db 74 KVDDTFYYV 82

## RESULT 7

Q49QR1\_9POXV

ID Q49QR1\_9POXV PRELIMINARY; PRT; 150 AA.  
AC Q49QR1;  
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.  
DT 13-SEP-2005, sequence version 1.  
DT 07-FEB-2006, entry version 6.  
DE Hypothetical protein.  
GN ORFNames=m8020L, m0020L;  
OS Vaccinia virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10245;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=LC16m8, and LC16m0;  
RX PubMed=16140764; DOI=10.1128/JVI.79.18.11873-11891.2005;  
RA Morikawa S., Sakiyama T., Hasegawa H., Saijo M., Maeda A., Kurane I.,  
RA Maeno G., Kimura J., Hiramata C., Yoshida T., Asahi-Ozaki Y., Sata T.,  
RA Kurata T., Kojima A.;  
RT "An attenuated LC16m8 smallpox vaccine: analysis of full-genome  
RT sequence and induction of immune protection.";  
RL J. Virol. 79:11873-11891(2005).  
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CC -----  
DR EMBL; AY678275; AAW23413.1; -; Genomic\_DNA.  
DR EMBL; AY678277; AAW23695.1; -; Genomic\_DNA.  
DR GO; GO:0016032; P:viral life cycle; IEA.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
|||||  
Db 74 KVDDTFYYV 82

## RESULT 8

Q6RZS8\_9POXV

ID Q6RZS8\_9POXV PRELIMINARY; PRT; 150 AA.  
AC Q6RZS8;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE RPXV013.  
GN ORFNames=RPXV013;  
OS Rabbitpox virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=32606;

RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=16227218; DOI=10.1099/vir.0.81331-0;  
RA Li G., Chen N., Roper R.L., Feng Z., Hunter A., Danila M.,  
RA Lefkowitz E.J., Buller R.M., Upton C.;  
RT "Complete coding sequences of the rabbitpox virus genome.";  
RL J. Gen. Virol. 86:2969-2977(2005).  
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CC -----  
DR EMBL; AY484669; AAS49726.1; -; Genomic\_DNA.  
DR GO; GO:0016032; P:viral life cycle; IEA.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
|||  
Db 74 KVDDTFYYV 82

## RESULT 9

## Q76Q66\_VARV

ID Q76Q66\_VARV PRELIMINARY; PRT; 150 AA.  
AC Q76Q66;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE B14L protein.  
GN Name=B14L;  
OS Variola minor virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=53258;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Garcia-1966;  
RA Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F.,  
RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,  
RA Esposito J.J., Sosnovtsev S.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.  
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CC -----  
DR EMBL; Y16780; CAB54608.1; -; Genomic\_DNA.  
DR GO; GO:0016032; P:viral life cycle; IEA.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
SQ SEQUENCE 150 AA; 18027 MW; 50FDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
|||

Db 74 KVDDTFYYV 82

## RESULT 10

Q76QL6\_COWPX

ID Q76QL6\_COWPX PRELIMINARY; PRT; 150 AA.  
 AC Q76QL6;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 9.  
 DE C13L protein.  
 GN Name=C13L;  
 OS Cowpox virus (CPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=10243;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GRI-90;  
 RX MEDLINE=97068532; PubMed=8963248;  
 RA Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,  
 RA Shchelkunov S.N., Sandakhchiev L.S.;  
 RT "Genes of a circle of hosts for the cowpox virus.";  
 RL Dokl. Akad. Nauk SSSR 349:829-833(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GRI-90;  
 RX MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;  
 RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,  
 RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;  
 RT "The genomic sequence analysis of the left and right species-specific  
 RT terminal region of a cowpox virus strain reveals unique sequences and  
 RT a cluster of intact ORFs for immunomodulatory and host range  
 RT proteins.";  
 RL Virology 243:432-460(1998).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GRI-90;  
 RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,  
 RA Ryazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,  
 RA Sandakhchiev L.S.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
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 CC -----  
 DR EMBL; X94355; CAA64098.1; -; Genomic\_DNA.  
 DR GO; GO:0016032; P:viral life cycle; IEA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
 |||||  
 Db 74 KVDDTFYYV 82

## RESULT 11

Q77TN9\_VACCT

ID Q77TN9\_VACCT PRELIMINARY; PRT; 150 AA.  
AC Q77TN9;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE TC7L.  
OS Vaccinia virus (strain Tian Tan) (VACV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10253;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Tian Tan;  
RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,  
RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;  
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.  
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CC -----  
DR EMBL; AF095689; AAF33872.1; -; Genomic\_DNA.  
DR GO; GO:0016032; P:viral life cycle; IEA.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
|||||||  
Db 74 KVDDTFYYV 82

## RESULT 12

## Q8JLI7\_9POXV

ID Q8JLI7\_9POXV PRELIMINARY; PRT; 150 AA.  
AC Q8JLI7;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE EVM015.  
GN Name=EVM015;  
OS Ectromelia virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=12643;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Moscow;  
RX MEDLINE=95266283; PubMed=7747448;  
RA Mossman K., Upton C., Buller R.M., McFadden G.;  
RT "Species specificity of ectromelia virus and vaccinia virus  
RT interferon-gamma binding proteins.";  
RL Virology 208:762-769(1995).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Moscow;  
RX MEDLINE=20192152; PubMed=10725549; DOI=10.1016/S0168-1702(99)00135-5;  
RA Chen N., Buller R.M., Wall E.M., Upton C.;  
RT "Analysis of host response modifier ORFs of ectromelia virus, the  
RT causative agent of mousepox.";

RL Virus Res. 66:155-173(2000).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Moscow;  
 RX MEDLINE=98154919; PubMed=9495531; DOI=10.1016/S0168-1702(97)00122-6;  
 RA Wall E.M., Cao J.X., Chen N., Buller R.M.L., Upton C.;  
 RT "A novel poxvirus gene and its human homolog are similar to an E. coli  
 RT lysophospholipase.";  
 RL Virus Res. 52:157-167(1997).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Moscow;  
 RA Chen N., Danila M.I., Feng Z., Buller M.L., Wang C., Han X.,  
 RA Lefkowitz E., Upton C.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
 CC -----  
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 CC -----  
 DR EMBL; AF012825; AAM92321.1; -; Genomic\_DNA.  
 DR GO; GO:0016032; P:viral life cycle; IEA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 SQ SEQUENCE 150 AA; 18130 MW; 4DD4FC55F62422BE CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
 |||||  
 Db 74 KVDDTFYYV 82

## RESULT 13

## Q8QN33\_COWPX

ID Q8QN33\_COWPX PRELIMINARY; PRT; 150 AA.  
 AC Q8QN33;  
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE CPXV029 protein.  
 GN Name=CPXV029 CDS;  
 OS Cowpox virus (CPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=10243;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Brighton Red;  
 RX MEDLINE=83117629; PubMed=6961398;  
 RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;  
 RT "Sequence of terminal regions of cowpox virus DNA: arrangement of  
 RT repeated and unique sequence elements.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Brighton Red;  
 RX MEDLINE=90177240; PubMed=2309453;  
 RA Parsons B.L., Pickup D.J.;  
 RT "Transcription of orthopoxvirus telomeres at late times during  
 RT infection.";  
 RL Virology 175:69-80(1990).



RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Brighton Red;  
RX MEDLINE=91196263; PubMed=2014645;  
RA Hu F.Q., Pickup D.J.;  
RT "Transcription of the terminal loop region of vaccinia virus DNA is  
RT initiated from the telomere sequences directing DNA resolution.";  
RL Virology 181:716-720(1991).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Brighton Red;  
RX MEDLINE=94378510; PubMed=8091665;  
RA Hu F.Q., Smith C.A., Pickup D.J.;  
RT "Cowpox virus contains two copies of an early gene encoding a soluble  
RT secreted form of the type II TNF receptor.";  
RL Virology 204:343-356(1994)..  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Brighton Red;  
RA Dietrich F.S., Ray C.A., Sharma D.A., Allen A., Pickup D.J.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; AF482758; AAM13476.1; -; Genomic DNA.  
DR GO; GO:0016032; P:viral life cycle; IEA.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
SQ SEQUENCE 150 AA; 17954 MW; 6B5C029714B02944 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
|||  
Db 74 KVDDTFYYV 82

## RESULT 14

## Q4WIR3\_ASPFU

ID Q4WIR3\_ASPFU PRELIMINARY; PRT; 512 AA.  
AC Q4WIR3;  
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2005, sequence version 1.  
DT 07-MAR-2006, entry version 6.  
DE Possible beta-xylosidase, family 43 of glycosyl hydrolases.  
GN ORFNames=Afu2g00930;  
OS Aspergillus fumigatus (Sartorya fumigata).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI\_TaxID=5085;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Af293 / CBS 101355 / FGSC A1100;  
RX PubMed=16372009; DOI=10.1038/nature04332;  
RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,  
RA Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,  
RA Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,  
RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,  
RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,  
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,

RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,  
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,  
 RA Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,  
 RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,  
 RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,  
 RA Penalva M.A., Perteau M., Price C., Pritchard B.L., Quail M.A.,  
 RA Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,  
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,  
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
 RA Takeuchi M., Tekaiia F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,  
 RA Machida M., Hall N., Barrell B.G., Denning D.W.;  
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
 RT *Aspergillus fumigatus*.";  
 RL Nature 438:1151-1156(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 DR EMBL; AAHF01000008; EAL87192.1; -; Genomic\_DNA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 KW Complete proteome; Hydrolase.  
 SQ SEQUENCE 512 AA; 55648 MW; 5E174A037C55B830 CRC64;

Query Match 77.8%; Score 7; DB 2; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8  
 |||||  
 Db 26 VDDTFYY 32

## RESULT 15

## Q2U7D1\_ASPOR

ID Q2U7D1\_ASPOR PRELIMINARY; PRT; 515 AA.  
 AC Q2U7D1;  
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.  
 DT 24-JAN-2006, sequence version 1.  
 DT 07-MAR-2006, entry version 3.  
 DE Beta-xylosidase.  
 GN ORFNames=AO090701000886;  
 OS *Aspergillus oryzae*.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.  
 OX NCBI\_TaxID=5062;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=RIB 40;  
 RX PubMed=16372010; DOI=10.1038/nature04300;  
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,  
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,  
 RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,  
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,  
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,  
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,  
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,  
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,

RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
RA Kuhara S., Ogasawara N., Kikuchi H.;  
RT "Genome sequencing and analysis of *Aspergillus oryzae*.";  
RL Nature 438:1157-1161(2005).  
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CC -----  
DR EMBL; AP007164; BAE62534.1; -; Genomic\_DNA.  
SQ SEQUENCE 515 AA; 56635 MW; 3EDFD2B09FF52176 CRC64;

Query Match 77.8%; Score 7; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 7.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8  
      |||||  
Db 39 VDDTFYY 45

## RESULT 16

P73845\_SYNY3

ID P73845\_SYNY3 PRELIMINARY; PRT; 770 AA.  
AC P73845;  
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.  
DT 01-FEB-1997, sequence version 1.  
DT 07-FEB-2006, entry version 26.  
DE Sll1608 protein.  
GN OrderedLocusNames=sll1608;  
OS Synechocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=97061201; PubMed=8905231; DOI=10.1093/dnares/3.3.109;  
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,  
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
RA Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
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CC -----  
DR EMBL; BA000022; BAA17904.1; -; Genomic\_DNA.  
DR PIR; S75042; S75042.  
DR BioCyc; SSP1148:SL1608-MONOMER; -.  
DR InterPro; IPR002931; Trnsglutase\_like.  
DR Pfam; PF01841; Transglut\_core; 1.  
DR SMART; SM00460; TGc; 1.  
KW Complete proteome.  
SQ SEQUENCE 770 AA; 87815 MW; F58C2EA34EC8873C CRC64;

Query Match 77.8%; Score 7; DB 2; Length 770;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8

Db                    |||||  
286 VDDTFYY 292

## RESULT 17

## Q8VUW8\_STAHO

ID Q8VUW8\_STAHO PRELIMINARY; PRT; 103 AA.  
AC Q8VUW8;  
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2002, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE ORF19.  
OS Staphylococcus hominis.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1290;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=GIFU12263;  
RX MEDLINE=22586405; PubMed=12700250;  
RX DOI=10.1128/JB.185.9.2711-2722.2003;  
RA Katayama Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,  
RA Kobayashi I., Hiramatsu K.;  
RT "Identification in methicillin-susceptible Staphylococcus hominis of  
RT an active primordial mobile genetic element for the staphylococcal  
RT cassette chromosome mec of methicillin-resistant Staphylococcus  
RT aureus.";  
RL J. Bacteriol. 185:2711-2722(2003).  
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CC -----  
DR EMBL; AB063171; BAB83490.1; -; Genomic\_DNA.  
DR InterPro; IPR009303; DUF960\_STA\_spp.  
DR Pfam; PF06124; DUF960; 1.  
SQ SEQUENCE 103 AA; 12599 MW; 13194326CCE4617D CRC64;

Query Match                    66.7%; Score 6; DB 2; Length 103;  
Best Local Similarity        100.0%; Pred. No. 30;  
Matches        6; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy                    4 DTFYYV 9  
                     |||||  
Db                    91 DTFYYV 96

## RESULT 18

## Q38248\_9CAUD

ID Q38248\_9CAUD PRELIMINARY; PRT; 126 AA.  
AC Q38248;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE DNA polymerase subunit.  
OS Lactococcus phage bIL67.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC c2-like viruses.  
OX NCBI\_TaxID=36343;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=95111629; PubMed=7812447;  
RA Schouler C., Ehrlich S.D., Chopin M.C.;  
RT "Sequence and organization of the lactococcal prolate-headed bIL67  
RT phage genome.";  
RL Microbiology 140:3061-3069(1994).

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CC -----  
DR EMBL; L33769; AAA74342.1; -; Genomic\_DNA.  
SQ SEQUENCE 126 AA; 14843 MW; 1768C9622ED7749B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 126;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTF 6  
|||  
Db 100 KVDDTF 105

## RESULT 19

## Q5A2T5\_CANAL

ID Q5A2T5\_CANAL PRELIMINARY; PRT; 176 AA.  
AC Q5A2T5;  
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.  
DT 26-APR-2005, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Hypothetical protein.  
GN ORFNames=CaO19.2181, CaO19.9727;  
OS Candida albicans SC5314.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=237561;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=SC5314;  
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,  
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,  
RA Davis R.W., Scherer S.;  
RT "The diploid genome sequence of Candida albicans."  
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC -----  
DR EMBL; AACQ01000075; EAK97013.1; -; Genomic\_DNA.  
DR EMBL; AACQ01000076; EAK96954.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 176 AA; 19448 MW; D04B9BE79CA86853 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 176;  
Best Local Similarity 100.0%; Pred. No. 45;

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006

## RESULT 6

## VHR2\_VARV

ID VHR2\_VARV STANDARD; PRT; 150 AA.  
AC P33860;  
DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.  
DT 01-FEB-1994, sequence version 1.  
DT 07-FEB-2006, entry version 30.  
DE Host range protein 2.  
GN ORFNames=C7L, B15L, D8L;  
OS Variola virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10255;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=India-1967 / Isolate Ind3;  
RX MEDLINE=93202281; PubMed=8384129; DOI=10.1016/0014-5793(93)80041-R;  
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;  
RT "Genes of variola and vaccinia viruses necessary to overcome the host  
RT protective mechanisms.";  
RL FEBS Lett. 319:80-83(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=Bangladesh-1975;  
RX MEDLINE=94088747; PubMed=8264798; DOI=10.1038/366748a0;  
RA Massung R.F., Esposito J.J., Liu L.I., Oi J., Utterback T.R.,  
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,  
RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,  
RA Venter C.J.;  
RT "Potential virulence determinants in terminal regions of variola  
RT smallpox virus genome.";  
RL Nature 366:748-751(1993).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=Congo-1965, Garcia-1966, and Somalia-1977;  
RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,  
RA Totmenin A.V., Shchelkunov S.N., Esposito J.J.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Plays a role for multiplication of the virus in  
CC different cell types (By similarity).  
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.  
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CC -----  
DR EMBL; X69198; CAA48949.1; -; Genomic\_DNA.  
DR EMBL; L22579; AAA60756.1; -; Genomic\_DNA.  
DR EMBL; U18340; AAA69419.1; -; Genomic\_DNA.  
DR EMBL; U18337; AAA69313.1; -; Genomic\_DNA.  
DR EMBL; U18338; AAA69354.1; -; Genomic\_DNA.  
DR PIR; F72151; F72151.  
DR PIR; H36837; H36837.  
DR PIR; T28446; T28446.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
FT CHAIN 1 150 Host range protein 2.  
FT /FTId=PRO\_0000099389.  
SQ SEQUENCE 150 AA; 18027 MW; 50FDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
|||  
Db 74 KVDDTFYYV 82

## RESULT 7

Q49QR1\_9POXV

ID Q49QR1\_9POXV PRELIMINARY; PRT; 150 AA.  
AC Q49QR1;  
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.  
DT 13-SEP-2005, sequence version 1.  
DT 07-FEB-2006, entry version 6.  
DE Hypothetical protein.  
GN ORFNames=m8020L, m0020L;  
OS Vaccinia virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10245;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=LC16m8, and LC16mO;  
RX PubMed=16140764; DOI=10.1128/JVI.79.18.11873-11891.2005;  
RA Morikawa S., Sakiyama T., Hasegawa H., Saijo M., Maeda A., Kurane I.,  
RA Maeno G., Kimura J., Hiramata C., Yoshida T., Asahi-Ozaki Y., Sata T.,  
RA Kurata T., Kojima A.;  
RT "An attenuated LC16m8 smallpox vaccine: analysis of full-genome  
RT sequence and induction of immune protection.";  
RL J. Virol. 79:11873-11891(2005).  
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CC -----  
DR EMBL; AY678275; AAW23413.1; -; Genomic\_DNA.  
DR EMBL; AY678277; AAW23695.1; -; Genomic\_DNA.  
DR GO; GO:0016032; P:viral life cycle; IEA.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
|||  
Db 74 KVDDTFYYV 82

## RESULT 8

Q6RZS8\_9POXV

ID Q6RZS8\_9POXV PRELIMINARY; PRT; 150 AA.  
AC Q6RZS8;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE RPXV013.  
GN ORFNames=RPXV013;  
OS Rabbitpox virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=32606;

RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=16227218; DOI=10.1099/vir.0.81331-0;  
 RA Li G., Chen N., Roper R.L., Feng Z., Hunter A., Danila M.,  
 RA Lefkowitz E.J., Buller R.M., Upton C.;  
 RT "Complete coding sequences of the rabbitpox virus genome.";  
 RL J. Gen. Virol. 86:2969-2977(2005).  
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 CC -----  
 DR EMBL; AY484669; AAS49726.1; -; Genomic\_DNA.  
 DR GO; GO:0016032; P:viral life cycle; IEA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;  
  
 Query Match 100.0%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
 |||||  
 Db 74 KVDDTFYYV 82

## RESULT 9

## Q76Q66\_VARV

ID Q76Q66\_VARV PRELIMINARY; PRT; 150 AA.  
 AC Q76Q66;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE B14L protein.  
 GN Name=B14L;  
 OS Variola minor virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=53258;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Garcia-1966;  
 RA Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F.,  
 RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,  
 RA Esposito J.J., Sosnovtsev S.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.  
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 DR EMBL; Y16780; CAB54608.1; -; Genomic\_DNA.  
 DR GO; GO:0016032; P:viral life cycle; IEA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 SQ SEQUENCE 150 AA; 18027 MW; 50FDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
 |||||



Db 74 KVDDTFYYV 82

## RESULT 10

Q76QL6\_COWPX

ID Q76QL6\_COWPX PRELIMINARY; PRT; 150 AA.  
 AC Q76QL6;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 9.  
 DE C13L protein.  
 GN Name=C13L;  
 OS Cowpox virus (CPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=10243;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GRI-90;  
 RX MEDLINE=97068532; PubMed=8963248;  
 RA Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,  
 RA Shchelkunov S.N., Sandakhchiev L.S.;  
 RT "Genes of a circle of hosts for the cowpox virus.";  
 RL Dokl. Akad. Nauk SSSR 349:829-833(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GRI-90;  
 RX MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;  
 RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,  
 RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;  
 RT "The genomic sequence analysis of the left and right species-specific  
 RT terminal region of a cowpox virus strain reveals unique sequences and  
 RT a cluster of intact ORFs for immunomodulatory and host range  
 RT proteins.";  
 RL Virology 243:432-460(1998).  
 RN [3]--  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GRI-90;  
 RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,  
 RA Ryazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,  
 RA Sandakhchiev L.S.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
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 DR EMBL; X94355; CAA64098.1; -; Genomic\_DNA.  
 DR GO; GO:0016032; P:viral life cycle; IEA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
 |||||  
 Db 74 KVDDTFYYV 82

## RESULT 11

Q77TN9\_VACCT

ID Q77TN9\_VACCT PRELIMINARY; PRT; 150 AA.  
AC Q77TN9;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE TC7L.  
OS Vaccinia virus (strain Tian Tan) (VACV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10253;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Tian Tan;  
RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,  
RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;  
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.  
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CC -----  
DR EMBL; AF095689; AAF33872.1; -; Genomic\_DNA.  
DR GO; GO:0016032; P:viral life cycle; IEA.  
DR InterPro; IPR004967; Pox\_C7\_F8A.  
DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
      |||||  
Db 74 KVDDTFYYV 82

## RESULT 12

Q8JLI7\_9POXV  
ID Q8JLI7\_9POXV PRELIMINARY; PRT; 150 AA.  
AC Q8JLI7;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE EVM015.  
GN Name=EVM015;  
OS Ectromelia virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=12643;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Moscow;  
RX MEDLINE=95266283; PubMed=7747448;  
RA Mossman K., Upton C., Buller R.M., McFadden G.;  
RT "Species specificity of ectromelia virus and vaccinia virus  
RT interferon-gamma binding proteins.";  
RL Virology 208:762-769(1995).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Moscow;  
RX MEDLINE=20192152; PubMed=10725549; DOI=10.1016/S0168-1702(99)00135-5;  
RA Chen N., Buller R.M., Wall E.M., Upton C.;  
RT "Analysis of host response modifier ORFs of ectromelia virus, the  
RT causative agent of mousepox.";

RL Virus Res. 66:155-173(2000).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Moscow;  
 RX MEDLINE=98154919; PubMed=9495531; DOI=10.1016/S0168-1702(97)00122-6;  
 RA Wall E.M., Cao J.X., Chen N., Buller R.M.L., Upton C.;  
 RT "A novel poxvirus gene and its human homolog are similar to an E. coli  
 RT lysophospholipase.";  
 RL Virus Res. 52:157-167(1997).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Moscow;  
 RA Chen N., Danila M.I., Feng Z., Buller M.L., Wang C., Han X.,  
 RA Lefkowitz E., Upton C.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
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 DR EMBL; AF012825; AAM92321.1; -; Genomic\_DNA.  
 DR GO; GO:0016032; P:viral life cycle; IEA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 SQ SEQUENCE 150 AA; 18130 MW; 4DD4FC55F62422BE CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9  
 |||||  
 Db 74 KVDDTFYYV 82

## RESULT 13

## Q8QN33\_COWPX

ID Q8QN33\_COWPX PRELIMINARY; PRT; 150 AA.  
 AC Q8QN33;  
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE CPXV029 protein.  
 GN Name=CPXV029 CDS;  
 OS Cowpox virus (CPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=10243;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Brighton Red;  
 RX MEDLINE=83117629; PubMed=6961398;  
 RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;  
 RT "Sequence of terminal regions of cowpox virus DNA: arrangement of  
 RT repeated and unique sequence elements.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Brighton Red;  
 RX MEDLINE=90177240; PubMed=2309453;  
 RA Parsons B.L., Pickup D.J.;  
 RT "Transcription of orthopoxvirus telomeres at late times during  
 RT infection.";  
 RL Virology 175:69-80(1990).

RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Brighton Red;  
 RX MEDLINE=91196263; PubMed=2014645;  
 RA Hu F.Q., Pickup D.J.;  
 RT "Transcription of the terminal loop region of vaccinia virus DNA is  
 RT initiated from the telomere sequences directing DNA resolution.";  
 RL Virology 181:716-720(1991).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Brighton Red;  
 RX MEDLINE=94378510; PubMed=8091665;  
 RA Hu F.Q., Smith C.A., Pickup D.J.;  
 RT "Cowpox virus contains two copies of an early gene encoding a soluble  
 RT secreted form of the type II TNF receptor.";  
 RL Virology 204:343-356(1994).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Brighton Red;  
 RA Dietrich F.S., Ray C.A., Sharma D.A., Allen A., Pickup D.J.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
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 DR EMBL; AF482758; AAM13476.1; -; Genomic\_DNA.  
 DR GO; GO:0016032; P:viral life cycle; IEA.  
 DR InterPro; IPR004967; Pox\_C7\_F8A.  
 DR Pfam; PF03287; Pox\_C7\_F8A; 1.  
 DR PIRSF; PIRSF003779; VAC\_C7L; 1.  
 SQ SEQUENCE 150 AA; 17954 MW; 6B5C029714B02944 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9  
 |||||  
 Db 74 KVDDTFYYV 82

## RESULT 14

## Q4WIR3\_ASPFU

ID Q4WIR3\_ASPFU PRELIMINARY; PRT; 512 AA.  
 AC Q4WIR3;  
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2005, sequence version 1.  
 DT 07-MAR-2006, entry version 6.  
 DE Possible beta-xylosidase, family 43 of glycosyl hydrolases.  
 GN ORFNames=Afu2g00930;  
 OS *Aspergillus fumigatus* (Sartorya fumigata).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.  
 OX NCBI\_TaxID=5085;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Af293 / CBS 101355 / FGSC A1100;  
 RX PubMed=16372009; DOI=10.1038/nature04332;  
 RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,  
 RA Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,  
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,  
 RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,  
 RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,  
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,

RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,  
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,  
 RA Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,  
 RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,  
 RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,  
 RA Penalva M.A., Perteau M., Price C., Pritchard B.L., Quail M.A.,  
 RA Rabbinoiwitsch E., Rawlins N., Rajandream M.A., Reichard U.,  
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,  
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
 RA Takeuchi M., Tekaiia F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,  
 RA Machida M., Hall N., Barrell B.G., Denning D.W.;  
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
 RT *Aspergillus fumigatus*.";   
 RL Nature 438:1151-1156(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 DR EMBL; AAHF01000008; EAL87192.1; -; Genomic\_DNA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 KW Complete proteome; Hydrolase.  
 SQ SEQUENCE 512 AA; 55648 MW; 5E174A037C55B830 CRC64;

Query Match 77.8%; Score 7; DB 2; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFYY 8  
 |||||  
 Db 26 VDDTFYY 32

## RESULT 15

Q2U7D1\_ASPOR

ID Q2U7D1\_ASPOR PRELIMINARY; PRT; 515 AA.

AC Q2U7D1;

DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.

DT 24-JAN-2006, sequence version 1.

DT 07-MAR-2006, entry version 3.

DE Beta-xylosidase.

GN ORFNames=AO090701000886;

OS *Aspergillus oryzae*.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.

OX NCBI\_TaxID=5062;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=RIB 40;

RX PubMed=16372010; DOI=10.1038/nature04300;

RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,

RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,

RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,

RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,

RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,

RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,

RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,

RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
RA Kuhara S., Ogasawara N., Kikuchi H.;  
RT "Genome sequencing and analysis of *Aspergillus oryzae*.";  
RL Nature 438:1157-1161(2005).  
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CC -----  
DR EMBL; AP007164; BAE62534.1; -; Genomic\_DNA.  
SQ SEQUENCE 515 AA; 56635 MW; 3EDFD2B09FF52176 CRC64;

Query Match 77.8%; Score 7; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 7.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8  
      |||||  
Db 39 VDDTFYY 45

## RESULT 16

P73845\_SYNY3

ID P73845\_SYNY3 PRELIMINARY; PRT; 770 AA.  
AC P73845;  
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.  
DT 01-FEB-1997, sequence version 1.  
DT 07-FEB-2006, entry version 26.  
DE Sll1608 protein.  
GN OrderedLocusNames=sll1608;  
OS *Synechocystis* sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; *Synechocystis*.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=97061201; PubMed=8905231; DOI=10.1093/dnares/3.3.109;  
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
RA Miyajima N., Hiroseawa M., Sugiura M., Sasamoto S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,  
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
RA Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
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CC -----  
DR EMBL; BA000022; BAA17904.1; -; Genomic\_DNA.  
DR PIR; S75042; S75042.  
DR BioCyc; SSP1148:SL1608-MONOMER; -.  
DR InterPro; IPR002931; Trnsglutumase\_like.  
DR Pfam; PF01841; Transglut\_core; 1.  
DR SMART; SM00460; TGc; 1.  
KW Complete proteome.  
SQ SEQUENCE 770 AA; 87815 MW; F58C2EA34EC8873C CRC64;

Query Match 77.8%; Score 7; DB 2; Length 770;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8

Db                    |||||  
286 VDDTFYY 292

## RESULT 17

## Q8VUW8\_STAHO

ID Q8VUW8\_STAHO PRELIMINARY; PRT; 103 AA.  
AC Q8VUW8;  
DT 01-MAR-2002; integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2002, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE ORF19.  
OS Staphylococcus hominis.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1290;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=GIFU12263;  
RX MEDLINE=22586405; PubMed=12700250;  
RX DOI=10.1128/JB.185.9.2711-2722.2003;  
RA Katayama Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,  
RA Kobayashi I., Hiramatsu K.;  
RT "Identification in methicillin-susceptible Staphylococcus hominis of  
RT an active primordial mobile genetic element for the staphylococcal  
RT cassette chromosome mec of methicillin-resistant Staphylococcus  
RT aureus.";  
RL J. Bacteriol. 185:2711-2722(2003).  
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CC -----  
DR EMBL; AB063171; BAB83490.1; -; Genomic\_DNA.  
DR InterPro; IPR009303; DUF960\_STA\_spp.  
DR Pfam; PF06124; DUF960; 1.  
SQ SEQUENCE 103 AA; 12599 MW; 13194326CCE4617D CRC64;

Query Match                    66.7%; Score 6; DB 2; Length 103;  
Best Local Similarity        100.0%; Pred. No. 30;  
Matches        6; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy                    4 DTFYYV 9  
                     |||||  
Db                    91 DTFYYV 96

## RESULT 18

## Q38248\_9CAUD

ID Q38248\_9CAUD PRELIMINARY; PRT; 126 AA.  
AC Q38248;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE DNA polymerase subunit.  
OS Lactococcus phage bIL67.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC c2-like viruses.  
OX NCBI\_TaxID=36343;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=95111629; PubMed=7812447;  
RA Schouler C., Ehrlich S.D., Chopin M.C.;  
RT "Sequence and organization of the lactococcal prolate-headed bIL67  
RT phage genome.";  
RL Microbiology 140:3061-3069(1994).

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CC -----  
DR EMBL; L33769; AAA74342.1; -; Genomic\_DNA.  
SQ SEQUENCE 126 AA; 14843 MW; 1768C9622ED7749B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 126;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTF 6 .  
|||  
Db 100 KVDDTF 105

## RESULT 19

## Q5A2T5\_CANAL

ID Q5A2T5\_CANAL PRELIMINARY; PRT; 176 AA.  
AC Q5A2T5;  
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.  
DT 26-APR-2005, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Hypothetical protein.  
GN ORFNames=CaO19.2181, CaO19.9727;  
OS Candida albicans SC5314.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=237561;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=SC5314;  
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,  
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,  
RA Davis R.W., Scherer S.;  
RT "The diploid genome sequence of Candida albicans.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC -----  
DR EMBL; AACQ01000075; EAK97013.1; -; Genomic\_DNA.  
DR EMBL; AACQ01000076; EAK96954.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 176 AA; 19448 MW; D04B9BE79CA86853 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 176;  
Best Local Similarity 100.0%; Pred. No. 45;

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